

FIG. 1

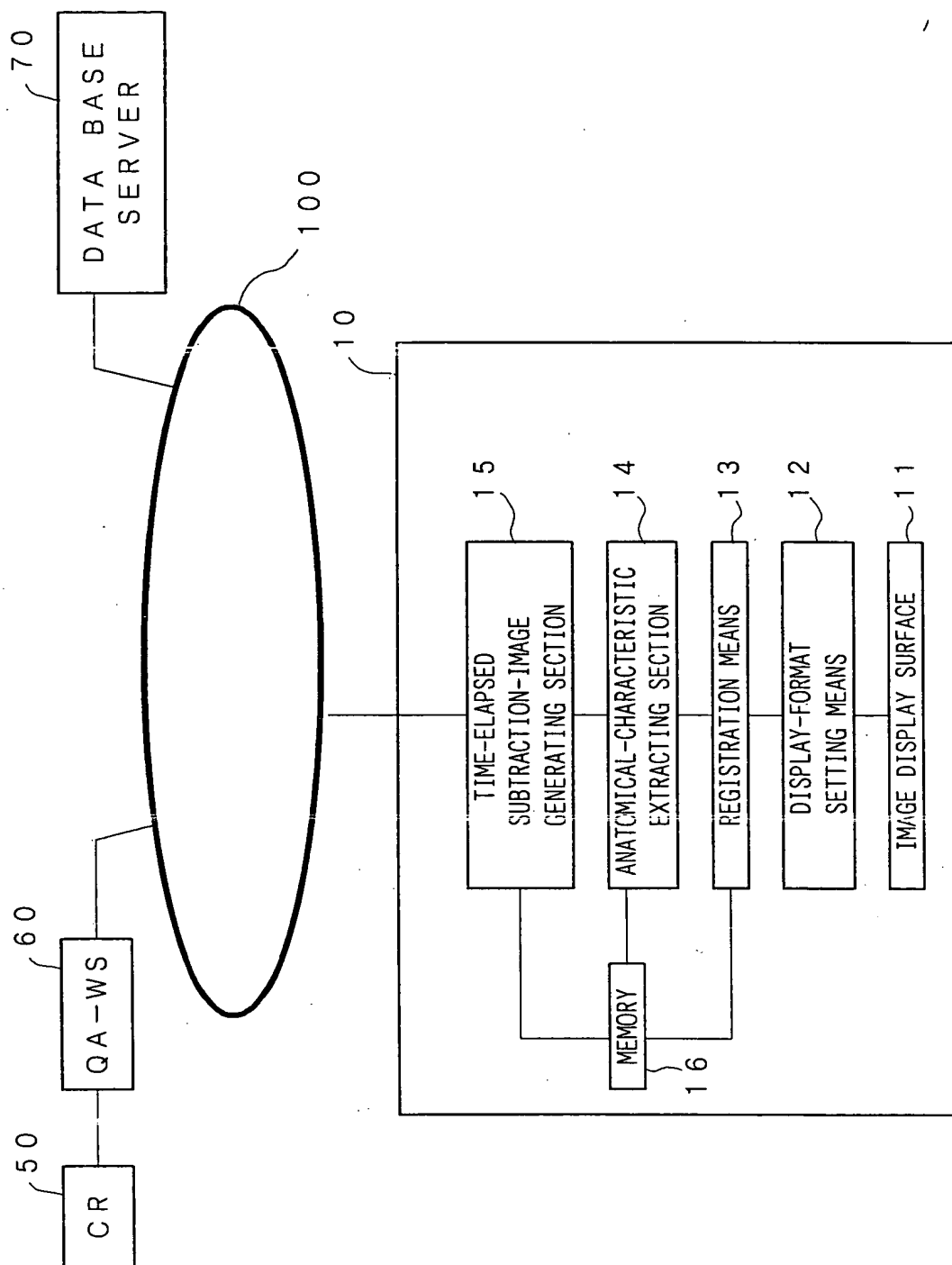
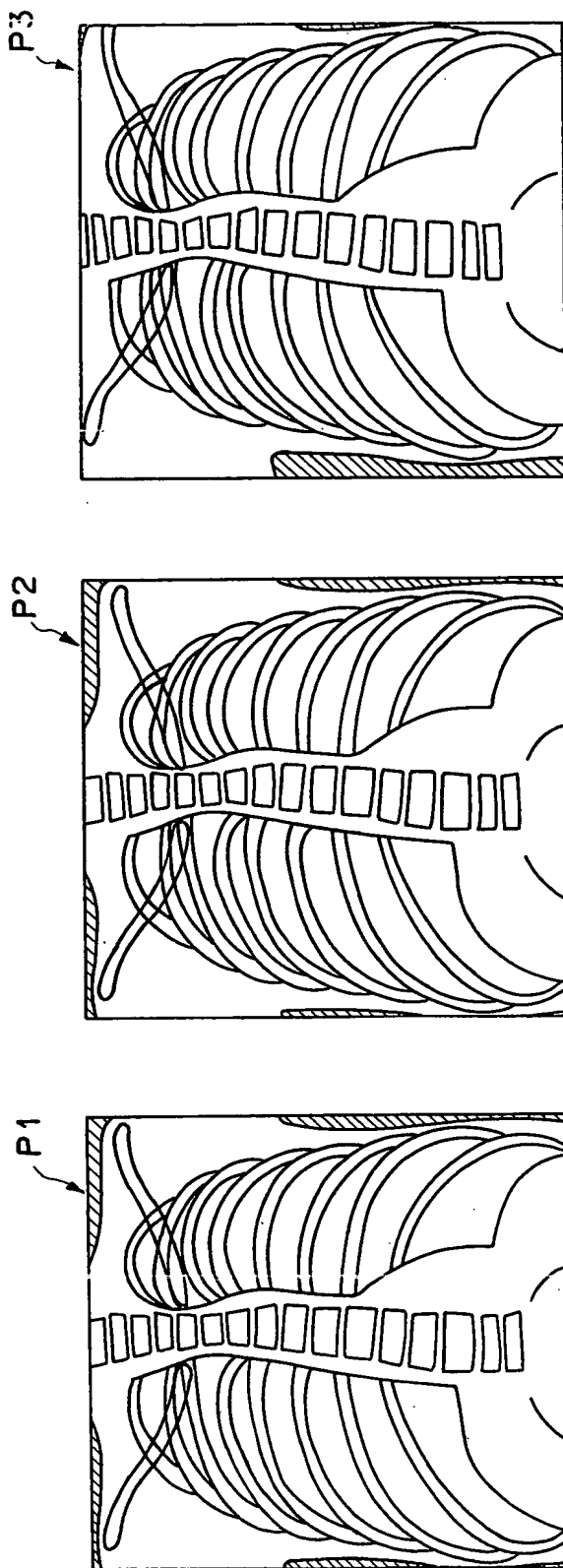


FIG. 2



FIRST ORIGINAL
IMAGE P1

THIRD ORIGINAL
IMAGE P3

GLOBAL MATCHING

$P1', P3$

- SETTING OF TEMPLATE ROI
(WITH RESPECT TO P3)
- SETTING OF SEARCH ROI
(WITH RESPECT TO P1')

DETERMINE SHIFT FOR
EACH ROI BY LOCAL MATCHING

APPROXIMATION OF A SHIFT
VALUES EMPLOYING A
TWO-DIMENSIONAL POLYNOMIAL
OF THE TENTH DEGREE

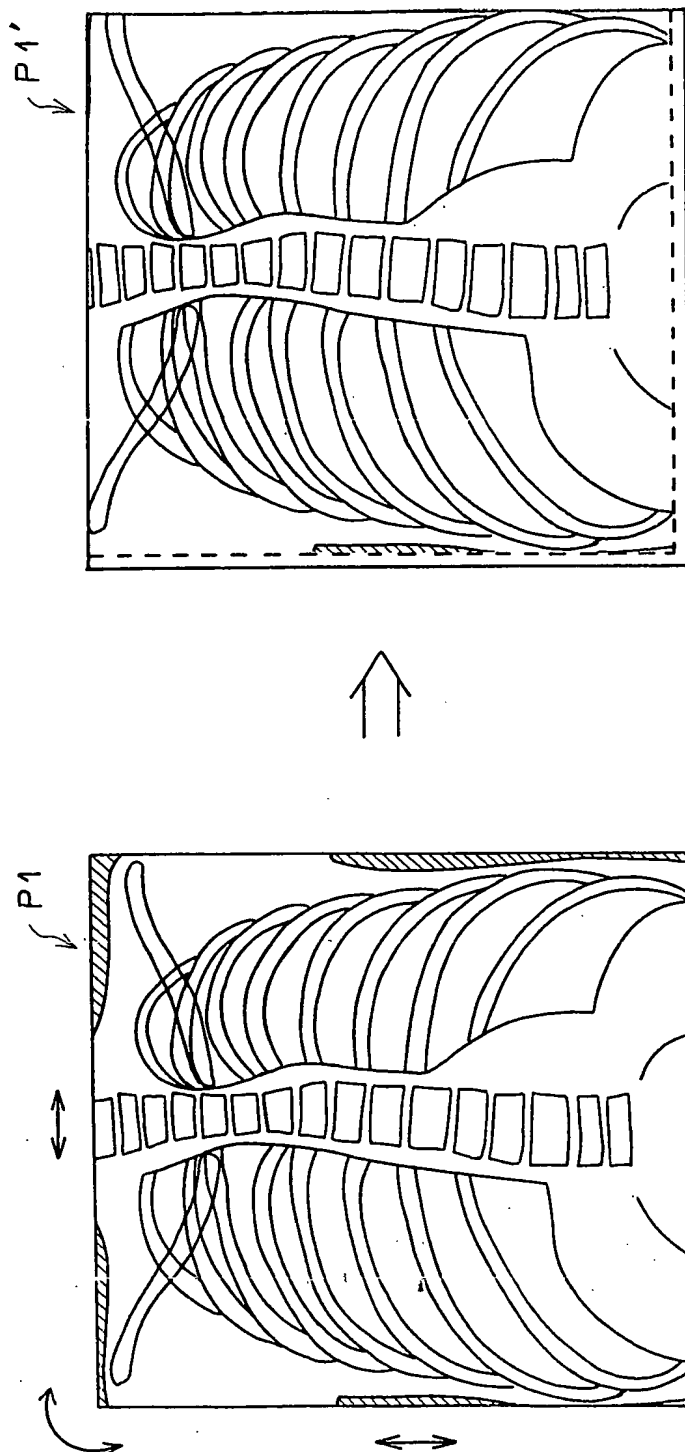
PERFORM A NON-LINEAR
WARPING PROCESS ON THE FIRST
IMAGE P'

$P1'', P3$

SUBTRACTION

$Su1$

FIG. 3



4-6-4

Figure 1. The 1000 most abundant genes in the *Salmonella* genome. The genes are arranged in descending order of abundance. The x-axis represents the number of genes, and the y-axis represents the number of genes per bin. The genes are grouped into bins of 100 genes each. The number of genes per bin is indicated by the height of the bars. The number of genes per bin is also indicated by the number of genes in the bin. The number of genes per bin is also indicated by the number of genes in the bin.

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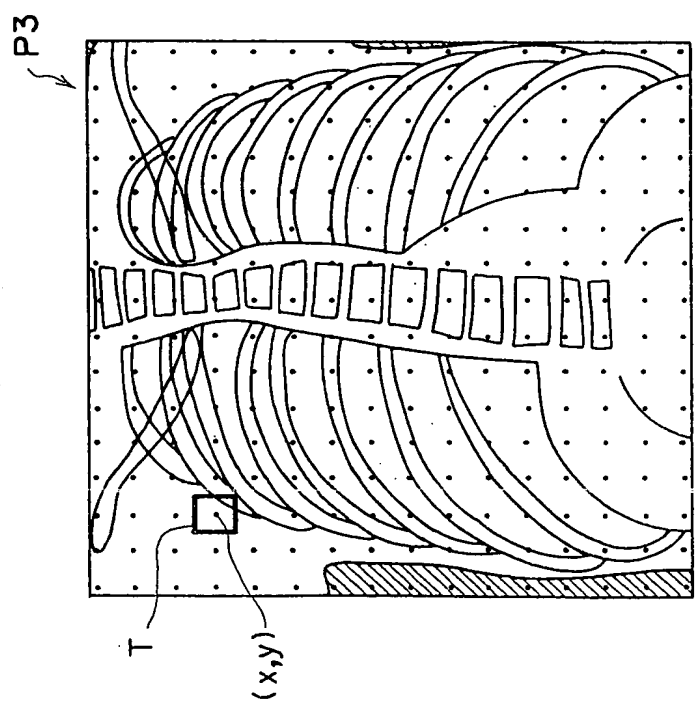
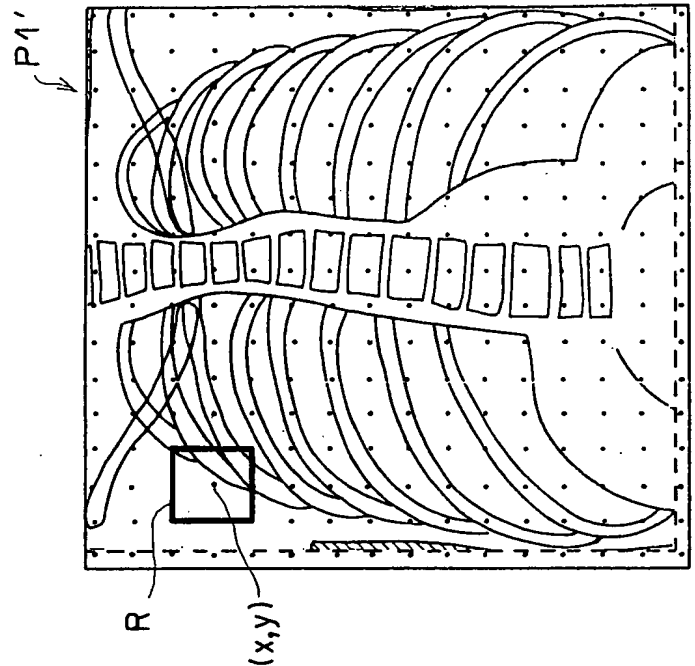
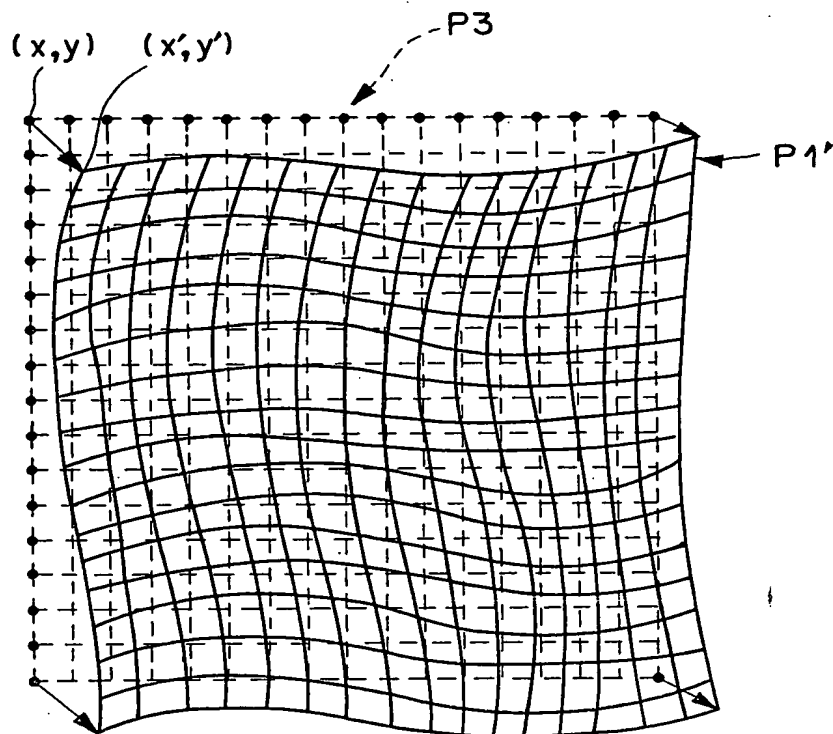


FIG. 5



F I G . 6

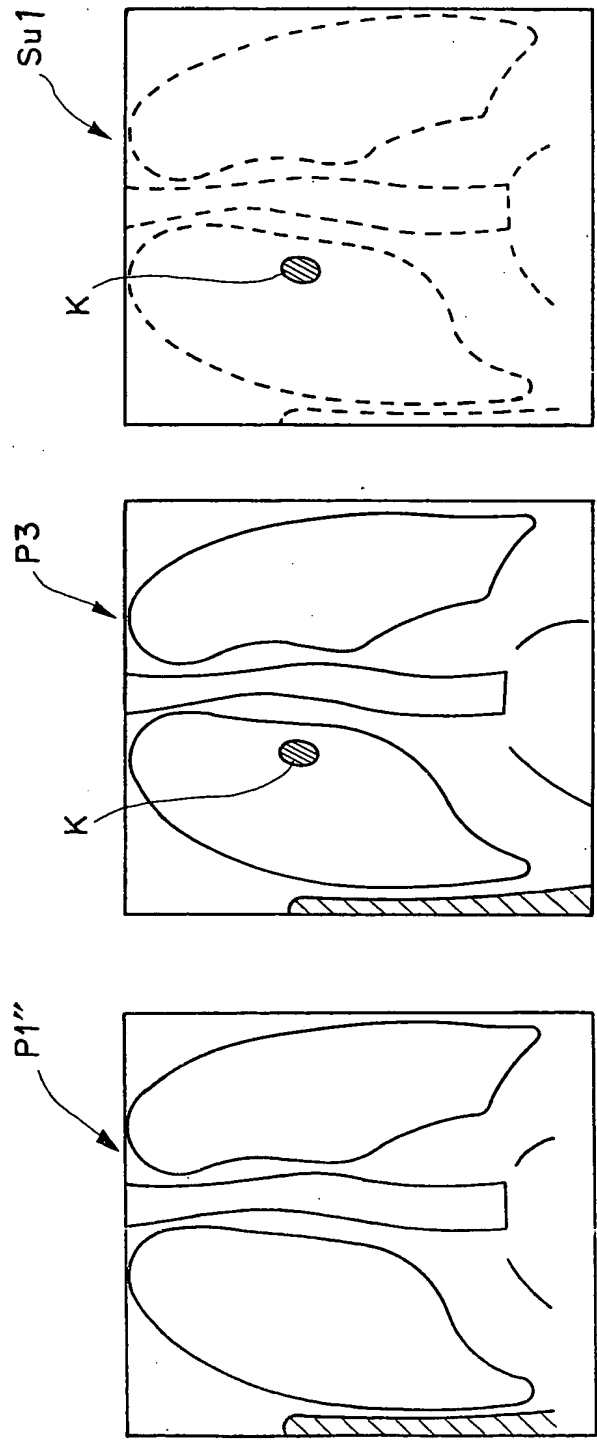
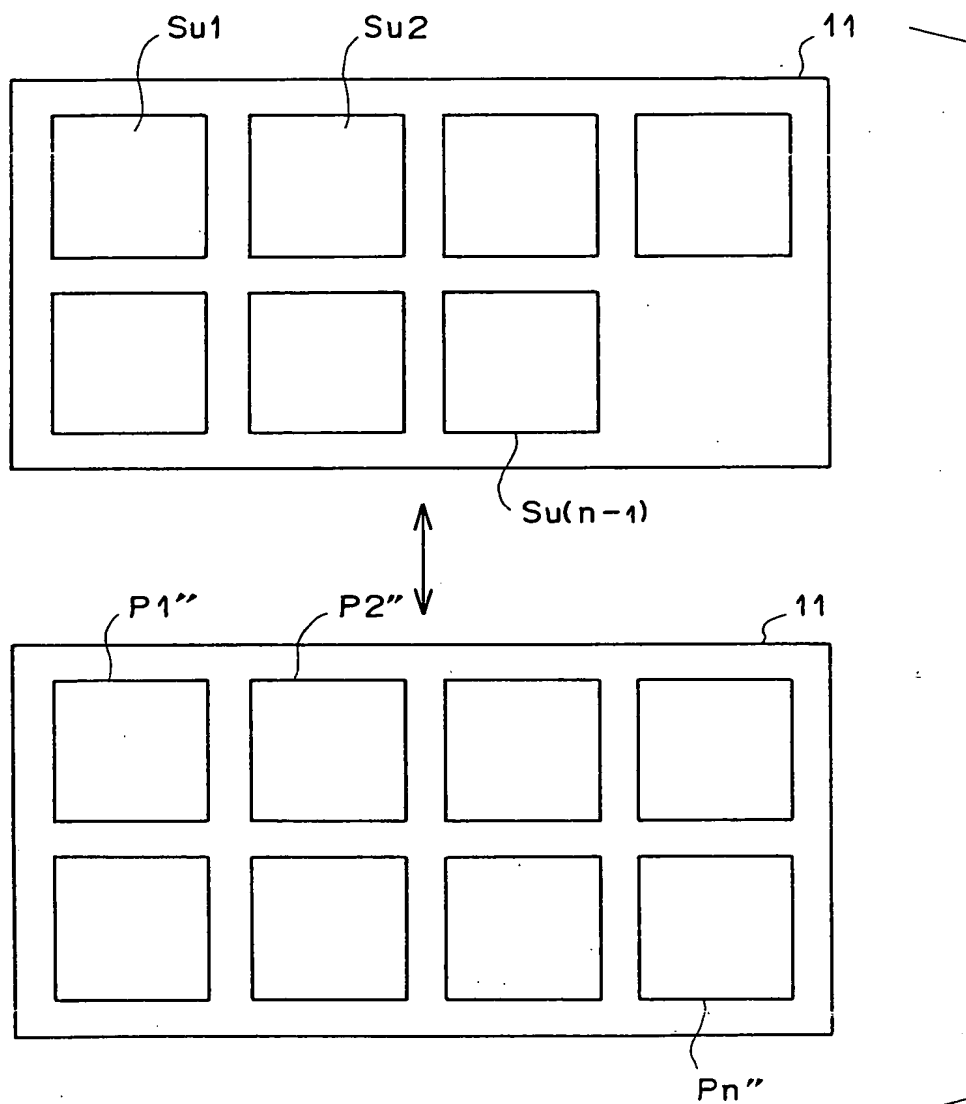


FIG. 7

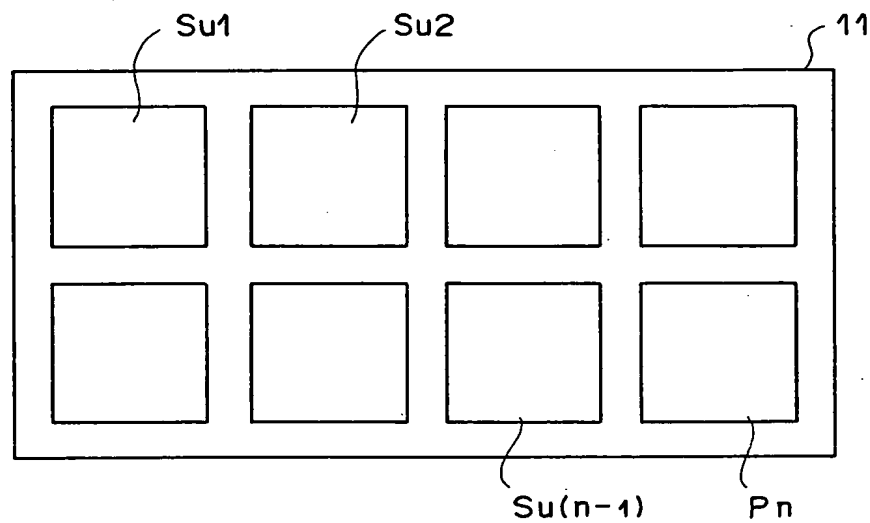


F I G . 9

BY DRAFTSMAN	CLASS	SUBCLASS
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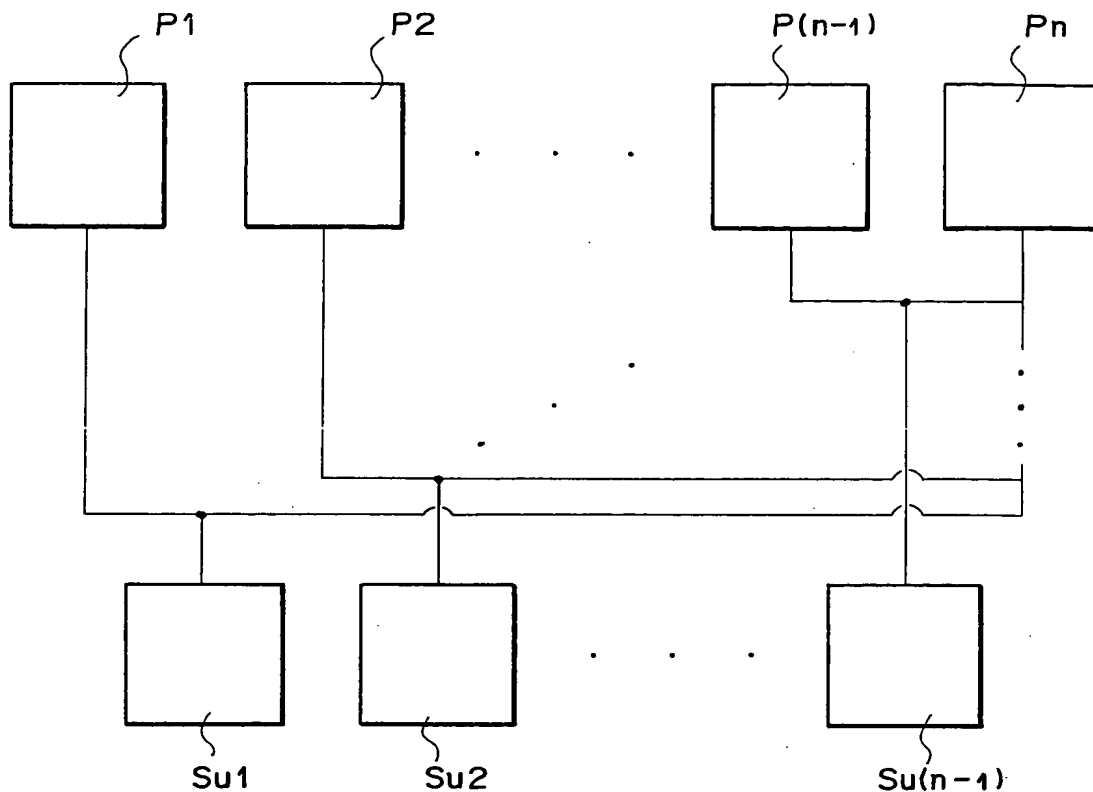
Akihiro Oosawa
 Date Filed: December 27, 2000
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 10 of 11

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F I G . 10

F I G . 11A



F I G . 11B

